ABSTRACT

The present invention compares expression profiles from matched samples to identify differential gene expression. Samples are matched according to physiological, pharmacological and/or disease state. Comparison of matched samples eliminates gene expression differences that are the result of changes in variables that are not of interest. The gene expression differences that remain can be attributed with a high degree of confidence to the unmatched variation. The gene expression differences thus identified can be used for example to diagnose disease, identify physiological state, design drugs, and monitor therapies.